




(FILE 'HOME' ENTERED AT 17:51:03 ON 22 FEB 2005)

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 17:51:05 ON 22 FEB 2005

L1	2192 S STREPTOMYCES (2N) AUREOFACIENS
L2	0 S L1 AND (HYDROXYBUTYRATE (3N) SYNTHASE)
L3	30 S L1 AND SYNTHASE
L4	12 DUP REM L3 (18 DUPLICATES REMOVED)
L5	12 S L1 AND (HYDROXYBUTYRATE OR PHB OR PHA OR POLYHYDROXYALKANOATE
L6	5 DUP REM L5 (7 DUPLICATES REMOVED)
L7	4 S NRRL2209
L8	2 DUP REM L7 (2 DUPLICATES REMOVED)

	Type	L #	Hits	Search Text
1	BRS	L1	2	"6756222"
2	BRS	L2	448	hydroxybutyrate and synthase
3	BRS	L3	34	l2 and aureofaciens
4	BRS	L4	40	hydroxybutyrate and aureofaciens
5	BRS	L5	10	phb and aureofaciens

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits Preview/Index History Clipboard Details

Range: from to Features: ☐ SNP ☐ CDD ☒ MGC ☐ HPRD

☐ 1: [AAK53451](#). Reports putative PHA synt...[gi:25989121] BLink, Links

LOCUS AAK53451 813 aa linear BCT 13-APR-2004
 DEFINITION putative PHA synthase [Streptomyces aureofaciens].
 ACCESSION AAK53451
 VERSION AAK53451.1 GI:25989121
 DBSOURCE accession [AY032926.1](#)
 KEYWORDS .
 SOURCE Streptomyces aureofaciens
 ORGANISM [Streptomyces aureofaciens](#)
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Streptomycineae; Streptomycetaceae; Streptomyces.
 REFERENCE 1 (residues 1 to 813)
 AUTHORS Mahishi,L.H., Tripathi,G., Ramachander,T.V.N. and Rawal,S.K.
 TITLE Cloning, molecular analysis and heterologous expression of the
 poly(3-hydroxybutyrate) synthesizing genes from Streptomyces
 aureofaciens NRRL 2209
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 813)
 AUTHORS Mahishi,L.H., Tripathi,G., Ramachander,T.N. and Rawal,S.K.
 TITLE Direct Submission
 JOURNAL Submitted (21-APR-2001) Plant Tissue Culture Division, National
 Chemical Laboratory, Pashan Road, Pune, Maharashtra 411008, India
 COMMENT Method: conceptual translation supplied by author.
 FEATURES Location/Qualifiers
 source 1..813
 /organism="Streptomyces aureofaciens"
 /strain="NRRL 2209"
 /db_xref="taxon:1894"
 Protein 1..813
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 /function="polymerization of hydroxyalkanoate monomers"
 CDS 1..813
 /gene="phaC"
 /coded_by="AY032926.1:2..2443"
 /transl_table=11

ORIGIN

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181 aavagawrap kgfartggav aglaavaavg gvpaaalpag wrvlayllcg laltavvrser
241 lpghaargvl aasgavvaga lvwalpp1aa vllgpvtvls dvwagtpdgf rsalgstlpw
301 selaaapvvl alvaghagge rnrrwpsvvr lrrrwpvlla rrrppgstgs gspghgcagr
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781 aspgrapvaw atqrarpsvr vgdgtgfept ssv

//

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Feb 9 2005 14:31:10

Database : A_Geneseq_16Dec04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query						Description
	No.	Score	Match	Length	DB	ID	
c	1	1267.5	14.5	19938	6	ABP76680	Abp76680 Streptomy
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	3	1113.5	12.1	19938	6	ABP76679	Abp76679 Streptomy
c	4	1107.5	12.7	19938	6	ABP76682	Abp76682 Streptomy
	5	1081.5	11.7	1953	6	AAE36881	Aae36881 Nephila m
c	6	1075	12.3	19938	6	ABP76681	Abp76681 Streptomy
c	7	1018.5	11.6	2294	7	ABO68485	Abo68485 Pseudomon
c	8	1013	11.6	1706	7	ABO83014	Abo83014 Pseudomon
	9	996.5	10.8	19938	6	ABP76680	Abp76680 Streptomy
c	10	995	11.4	1071	7	ADF94310	Adf94310 Human col
c	11	980.5	11.2	1064	2	AAR93254	Aar93254 Collagen-
c	12	980.5	11.2	1064	2	AAW57652	Aaw57652 Collagen-
c	13	980.5	11.2	1065	2	AAR37741	Aar37741 Collagen-
c	14	970.5	11.1	19938	6	ABB98398	Abb98398 Streptomy
	15	958.5	10.4	19938	6	ABB98398	Abb98398 Streptomy
	16	913.5	9.9	19938	6	ABP76681	Abp76681 Streptomy

Database : GenEmbl:*
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 2: gb_htg:*
 3: gb_in:*
 4: gb_om:*
 5: gb_ov:*
 6: gb_pat:*
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 9: gb_pr:*
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 11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	4824.4	100.0	4826	1	AY032926	AY032926 Streptomy
	3	1133	23.5	277000	1	SC0939109	AL939109 Streptomy
c	4	1096.4	22.7	299925	1	AP005048	AP005048 Streptomy
c	5	528	10.9	302007	1	SC0939132	AL939132 Streptomy
c	6	331.8	6.9	3030	8	VCA429230	AJ429230 Volvox ca
	7	314.4	6.5	167254	9	CNS05TDS	AL357093 Human chr
c	8	282.6	5.9	110000	1	AE000516_27	Continuation (28 o
c	9	282.6	5.9	346051	1	BX842580	BX842580 Mycobacte

12: geneseqn2004as:*

13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length	Match	Length			
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	3	294.4	6.1	114955	2	AAX53491			Aax53491 Human ade
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c	6	282.6	5.9	110000	4	AAI99683_27			Continuation (28 o
c	7	271.8	5.6	114955	2	AAX53491			Aax53491 Human ade
	8	262.6	5.4	110000	4	AAI99683_39			Continuation (40 o
	9	260.4	5.4	110000	4	AAI99682_39			Continuation (40 o
c	10	257.4	5.3	2543	12	ACH87341			Ach87341 Human gen
c	11	257	5.3	110000	4	AAI99683_06			Continuation (7 of
	12	255.4	5.3	3921	8	ACA40351			Aca40351 Prokaryot
c	13	255.4	5.3	110000	4	AAI99682_06			Continuation (7 of
c	14	253	5.2	110000	4	AAI99683_39			Continuation (40 o
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c	16	241.2	5.0	110000	4	AAI99682_37			Continuation (38 o
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Database : Issued_Patents_NA:*

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- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result		Query						Description
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c	3	282.6	5.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli	
	4	262.6	5.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli	
	5	260.4	5.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli	
c	6	188.2	3.9	6192	2	US-08-479-537A-1	Sequence 1, Appli	
c	7	188.2	3.9	6192	3	US-09-083-116-1	Sequence 1, Appli	
c	8	188.2	3.9	6192	3	US-09-134-916A-1	Sequence 1, Appli	
c	9	188.2	3.9	6449	2	US-08-479-537A-4	Sequence 4, Appli	
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c	11	188.2	3.9	6449	3	US-09-134-916A-4	Sequence 4, Appli	
	12	188	3.9	2457	4	US-09-863-859-21	Sequence 21, Appl	
	13	188	3.9	4881	4	US-09-863-859-23	Sequence 23, Appl	
	14	180	3.7	8438	1	US-07-945-283-1	Sequence 1, Appli	

Database : EST:*
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 4: gb_est3:*
 5: gb_est4:*
 6: gb_est5:*
 7: gb_est6:*
 8: gb_gss1:*
 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query						
No.	Score	Match	Length	DB	ID	Description		
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c	2	275.6	5.7	1695	8	CC290874	CC290874 CH261-172	
c	3	266.6	5.5	1674	9	CL078342	CL078342 CH216-149	
c	4	263.4	5.5	2332	9	AG363333	AG363333 Mus muscu	
	5	262.2	5.4	1956	9	CG754548	CG754548 P050-1-A1	
	6	261.6	5.4	1909	9	CL078604	CL078604 CH216-151	
	7	259.4	5.4	1628	9	CG757066	CG757066 P052-2-A0	
	8	258.2	5.4	1970	9	CG748837	CG748837 P042-4-E0	
	9	253	5.2	1738	9	CG750956	CG750956 P045-2-H0	
c	10	251.6	5.2	2198	9	AG332729	AG332729 Mus muscu	
	11	251	5.2	1839	9	CG747711	CG747711 P041-2-E0	
c	12	248.4	5.1	1788	8	CC320563	CC320563 TAM32-34P	
	13	247.4	5.1	1793	9	CG754612	CG754612 P050-1-D0	

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 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%							
Result			Query						
No.	Score	Match	Length	DB	ID			Description	
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c	2	841	9.6	924	2	S27923		gene LF3 protein -	
	3	829	9.0	1660	2	A70869		hypothetical glyci	
c	4	822	9.4	4776	2	E95206		cell wall surface	
	5	800	8.7	1489	2	D70807		hypothetical glyci	
	6	795	8.6	2639	2	T31328		fibroin - Chinese	
	7	791.5	8.6	1381	2	E70806		hypothetical glyci	
	8	791	8.6	1901	2	F70806		hypothetical glyci	
	9	781.5	8.5	1079	2	B70807		hypothetical glyci	
	10	777.5	8.4	1306	2	A70934		hypothetical glyci	
	11	776.5	8.4	1329	2	E70917		hypothetical glyci	
c	12	776.5	8.9	1344	1	A35175		mucin 1 precursor,	
	13	775	8.4	1466	1	CGHU7L		collagen alpha 1(I	
	14	774.5	8.4	13288	2	T03099		mucin, submaxillar	
	15	753	8.2	2944	2	A54849		collagen alpha 1(V	

Database : UniProt_03:*
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 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	3	1795	19.5	368	2	Q8GFF1 streptomyce
	4	1629	17.7	796	2	Q827V3 streptomyce
	5	1509	16.4	818	2	Q9F3E4 streptomyce
c	6	1351	15.4	263	2	Q8GFE8 streptomyce
c	7	1255	14.3	245	2	Q8GFF0 streptomyce
c	8	1133.5	13.0	3409	2	Q6SSE6 chlamydomon
c	9	1109.5	12.7	3889	2	Q6SSE8 chlamydomon
	10	1081.5	11.7	1953	2	Q9BIT7 nephila ina
c	11	1057.5	12.1	676	2	Q95JC9 sus scrofa
c	12	1020	11.7	190	2	Q8GFE9 streptomyce
	13	930.5	10.1	1884	2	Q9NHW2 nephila ina
c	14	914.5	10.5	7524	2	Q6PZE0 mus musculu
	15	891.5	9.7	2249	2	Q9NHW4 nephila cla
c	16	891	10.2	566	2	Q95JD1 sus scrofa
c	17	863.5	9.9	1188	2	Q41805 zea mays (m
c	18	841.5	9.6	2752	2	Q9UQ35 homo sapien